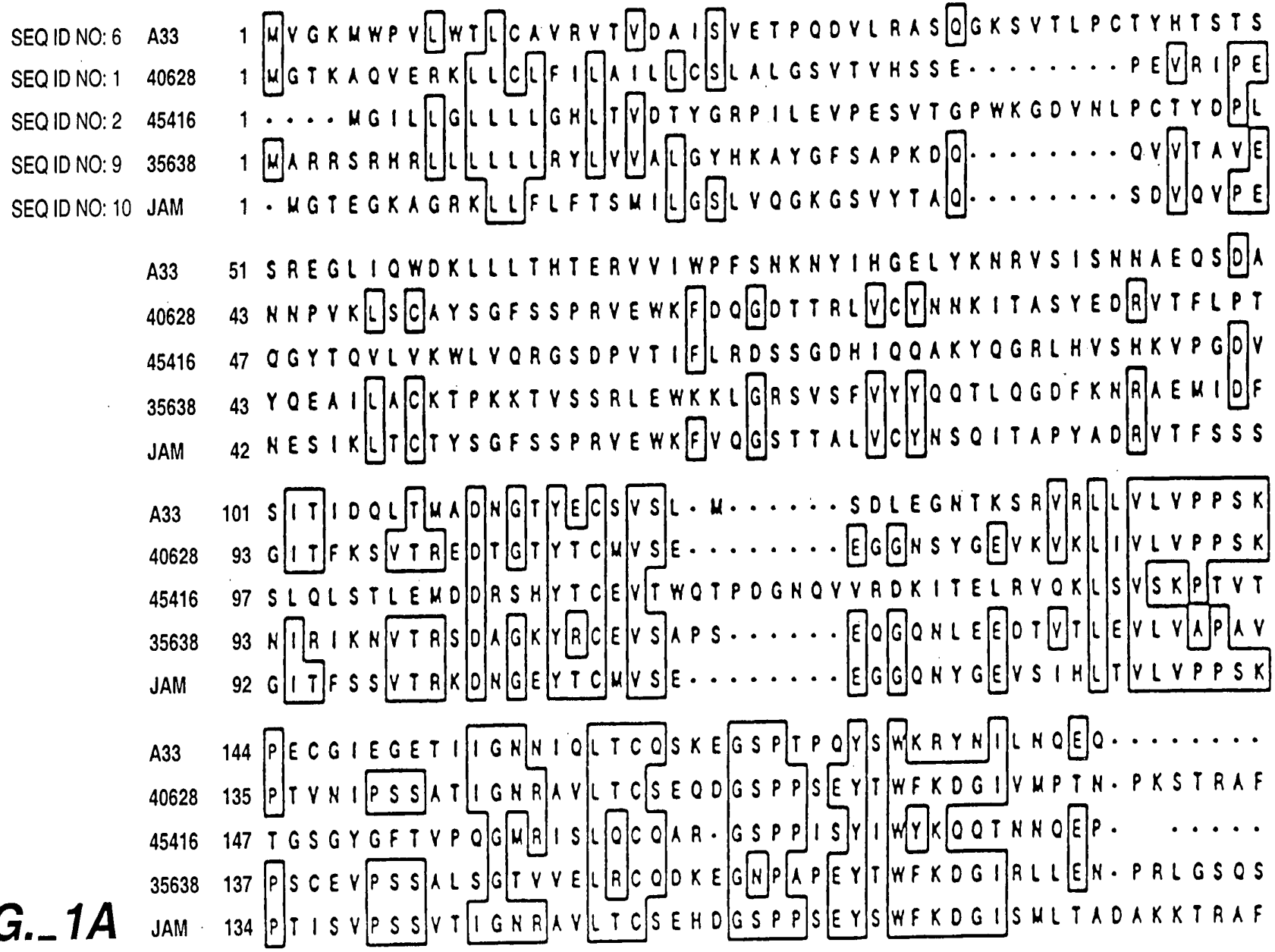
SEQ ID NO: 6 A33 1 MVGKMWPVLWTLCAVRVTVDAISVETPQDVLRASQGKSVTLPCTYHTSTS
SEQ ID NO: 1 40628 1 MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSE.....PEVRIPE
SEQ ID NO: 2 45416 1 ....MGILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPL
SEQ ID NO: 9 35638 1 MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQ.....QVVTAVE
SEQ ID NO: 10 JAM 1 .MGTEGKAGRKLLFLFTSMILGSLVQGKGSVYTAQ.....SDVQVPE
A33 51 SREGLIQWDKLLLTHTERVVIWPFSNKNYIHGELYKNRVSISNNAEQSDA
40628 43 NNPVKLSCAYSGFSSPRVEWKFDQGDTTRLVCYNNKITASYEDRVTFLPT
45416 47 QGYTQVLVKWLVQRGSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDV
35638 43 YQEAILACKTPKKTVSSRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDF
JAM 42 NESIKLTCTYSGFSSPRVEWKFVQGSTTALVCYNSQITAPYADRVTFSSS
A33 101 SITIDQLTMADNGTYECSVSL.M.....SDLEGNTKSRVRLLVLVPPSK
40628 93 GITFKSVTREDTGTYTCMVSE.....EGGNSYGEVKVKLIVLVPPSK
45416 97 SLQLSTLEMDDRSHYTCEVTWQTPDGNQVVRDKITELRVQKLSVSKPTVT
35638 93 NIRIKNVTRSDAGKYRCEVSAPS.....EQGQNLEEDTVTLEVLVAPAV
JAM 92 GITFSSVTRKDNGEYTCMVSE.....EGGQNYGEVSIHLTVLVPPSK
A33 144 PECGIEGETIIGNNIQLTCQSKEGSPTPQYSWKRYNILNQEQ.....
40628 135 PTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTN.PKSTRAF
45416 147 TGSGYGFTVPQGMRISLQCQAR.GSPPISYIWYKQQTNNQEP.....
35638 137 PSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLEN.PRLGSQS
JAM 134 PTISVPSSVTIGNRAVLTCSEHDGSPPSEYSWFKDGISMLTADAKKTRAF

FIG._1A

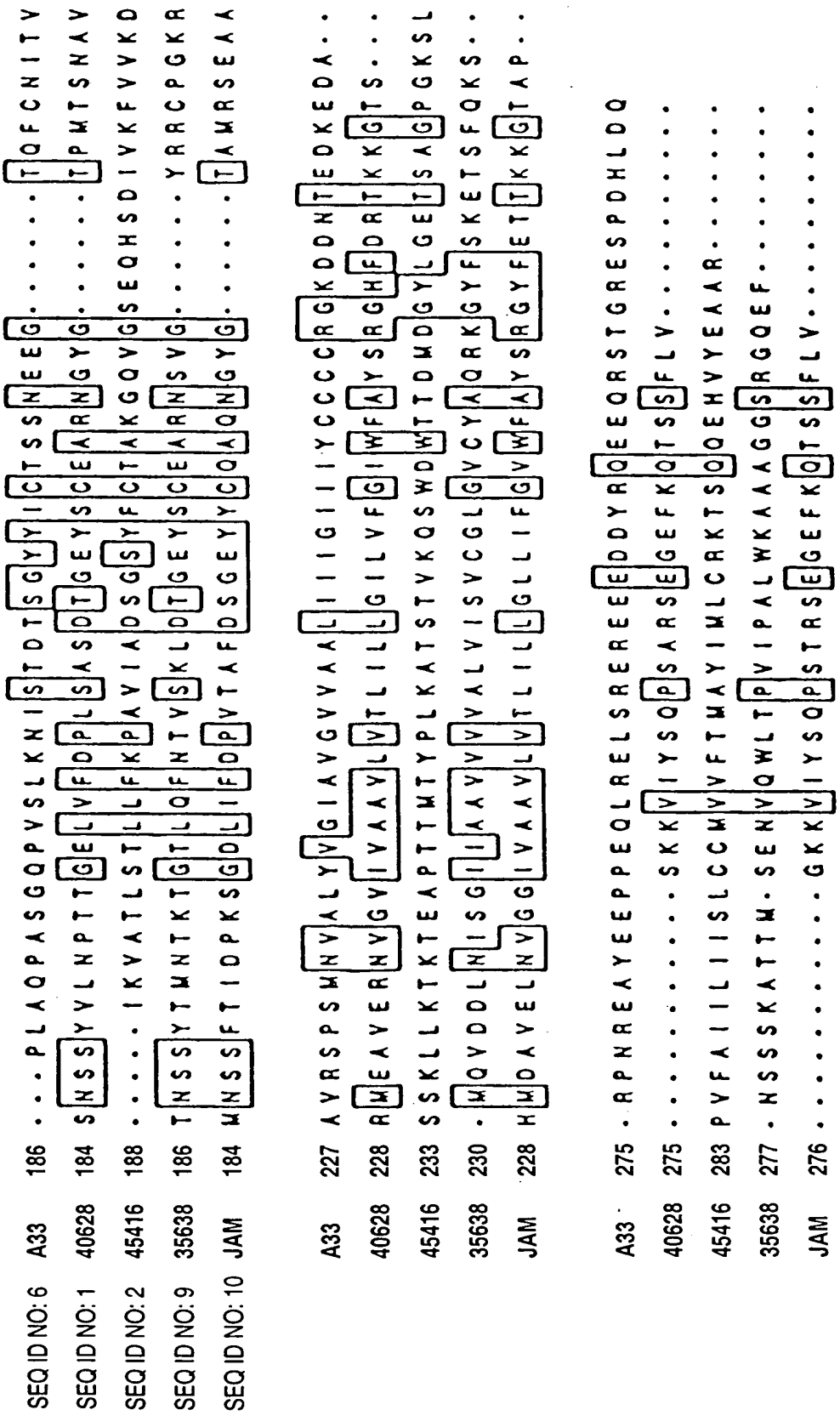
SEQ ID NO: 6 A33 186 . . . P L A Q P A S G Q P V S L K N I S T D T S G Y Y I C T S S N E E G . . . . . T Q F C N I T V
SEQ ID NO: 1 40628 184 S N S S Y Y L N P T T G E L V F D P L S A S D T G E Y S C E A R N G Y G . . . . . T P M T S N A V
SEQ ID NO: 2 45416 188 . . . . . I K V A T L S T L L L F K P A V I A D S G S Y F C T A K G Q V G S E Q H S D I V K F V V K D
SEQ ID NO: 9 35638 186 T N S S Y T M N T K T G T L Q F H T V S K L D T G E Y S C E A R N S V G . . . . . Y R R C P G K R
SEQ ID NO: 10 JAM 184 M N S S F T I D P K S G D L I F D P V T A F D S G E Y Y C Q A Q N G Y G . . . . . T A M R S E A A
A33 227 A V R S P S M N V A L Y V G I A V G V V A A L I I I G I I I Y C C C R G K D D N T E D K E D A . .
40628 228 R M E A Y E R N V G V I V A A Y L V T L I L L G I L V F G I W F A Y S R G H F D R T K K G T S . . .
45416 233 S S K L L K T K T E A P T T M T Y P L K A T S T V K Q S W D M T T D M D G Y L G E T S A G P G K S L
35638 230 . M Q V D D L N I S G I I A A Y V V V A L Y I S V C G L G V C Y A Q R K G Y F S K E T S F Q K S . .
JAM 228 H M D A Y E L N V G G I V A A Y L V T L I L L G L L I F G V W F A Y S R G Y F E T T K K G T A P . .
A33 275 . R P N R E A Y E E P P E Q L R E L S R E R E E E D D Y R Q E E Q R S T G R E S P D H L D Q
40628 275 . . . . . S K K V I Y S Q P S A R S E G E F K Q T S F L V . . . . . .
45416 283 P V F A I I L I I S L C C M V V F T M A Y I M L C R K T S Q Q E H V Y E A A R . . . . . .
35638 277 . N S S S K A T T M . S E N V Q W L T P V I P A L W K A A A G G S R G Q E F . . . . . .
JAM 276 . . . . . G K K V I Y S Q P S T R S E G E F K Q T S S F L V . . . . . .

FIG._1B

SEQ ID NO:1

```
Met Gly Thr Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe Ile Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr
 1               5                  10                  15                  20                  25                  30

Val His Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val
                35                  40                  45                  50                  55                  60

Glu Trp Lys Phe Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu
                65                  70                  75                  80                  85                  90

Pro Thr Gly Ile Thr Phe Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser Glu Glu Gly Gly Asn Ser Tyr Gly
                95                 100                 105                 110                 115                 120

Glu Val Lys Val Lys Leu Ile Val Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr Ile Gly Asn Arg Ala Val
               125                 130                 135                 140                 145                 150

Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn Pro Lys Ser Thr
               155                 160                 165                 170                 175                 180

Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly Glu Tyr
               185                 190                 195                 200                 205                 210

Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val
               215                 220                 225                 230                 235                 240

Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys
               245                 250                 255                 260                 265                 270

Lys Gly Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val
               275                 280                 285                 290                 295             299
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FIG._2

SEQ ID NO:2

1 MGILLGLLLL GHLTVDTYGR PILEVPESVT GPWKGDVNLP CTYDPLQGYT QVLVKWLVQR GSDPVTIFLR DSSGDHIQQA KYQGRLHVSH KVPGDVSLQL

101 STLEMDDRSH YTCEVTWQTP DGNQVVRDKI TELRVQKLSV SKPTVTTGSG YGFTVPQGMR ISLQCQARGS PPISYIWYKQ QTNNQEPIKV ATLSTLLFKP
^Glycosaminoglycan attachment site

201 AVIADSGSYF CTAKGQVGSE QHSDIVKFVV KDSSKLLKTK TEAPTTMTYP LKATSTVKQS WDWTTDMDGY LGETSAGPGK SLPVFAIILI ISLCCMVVFT
^Transmembrane domain

301 MAYIMLCRKT SQQEHVYEAA R

FIG._3

OLI2162 (35936.f1)
SEQ ID NO:12
TCGCGGAGCTGTGTTCTGTTTCCC

OLI2163 (35936.p1)
SEQ ID NO:13
TGATCGCGATGGGGACAAAGGCGCAAGCTCGAGAGGAAACTGTTGTGCCT

OLI2164 (35936.f2)
SEQ ID NO:14
ACACCTGGTTCAAAGATGGG

OLI2165 (35936.r1)
SEQ ID NO:15
TAGGAAGAGTTGCTGAAGGCACGG

OLI2166 (35936.f3)
SEQ ID NO:16
TTGCCTTACTCAGGTGCTAC

OLI2167 (35936.r2)
SEQ ID NO:17
ACTCAGCAGTGGTAGGAAAG

FIG._8

DNA35936 SEQ ID NO:3

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CTTCTTGCCA ACTGGTATCA CCTTCAAGTC CGTGACACGG GAAGACACTG 50
GGACATACAC TTGTATGGTC TCTGAGGAAG GCGGCAACAG CTATGGGGAG 100
GTCAAGGTCA AGCTCATCGT GCTTGTGCCT CCATCCAAGC CTACAGTTAA 150
CATCCCCTCC TCTGCCACCA TTGGGAACCG GGCAGTGCTG ACATGCTCAG 200
AACAAGATGG TTCCCCACCT TCTGAATACA CCTGGTTCAA AGATGGGATA 250
GTGATGCCTA CGAATCCCAA AAGCACCCGT GCCTTCAGCA ACTCTTCCTA 300
TGTCCTGAAT CCCACAACAG GAGAGCTGGT CTTTGATCCC CTGTCAGCCT 350
CTGATACTGG AGAATACAGC TGTGAGGCAC GGAATGGGTA 390
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FIG._4A

consen01 SEQ ID NO:4

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TCTCAGTCCC CTCGCTGTAG TCGCGGAGCT GTGTTCTGTT TCCCAGGAGT 50
CCTTCGGCGG CTGTTGTGCT CAGGTGCGCC TGATCGCGAT GGGGACAAAG 100
GCGCAAGCTC GAGAGGAAAC TGTTGTGCCT CTTCATATTG GCGATCCTGT 150
TGTGCTCCCT GGCATTGGGC AGTGTTACAG TTGCACTCTT CTGAACCTGA 200
AGTCAGAATT CCTGAGAATA ATCCTGTGAA GTTGTCCTGT GCCTACTCGG 250
GCTTTTCTTC TCCCCGTGTG GAGTGGAAGT TTGACCAAGG AGACACCACC 300
AGACTCGTTT GCTATAATAA CAAGATCACA GCTTCCTATG AGGACCGGGT 350
GACCTTCTTG CCAACTGGTA TCACCTTCAA GTCCGTGACA CGGGAAGACA 400
CTGGGACATA CACTTGTATG GTCTCTGAGG AAGGCGGCAA CAGCTATGGG 450
GAGGTCAAGG TCAAGCTCAT CGTGCTTGTG CCTCCATCCA AGCCTACAGT 500
TAACATCCCC TCCTCTGCCA CCATTGGGAA CCGGGCAGTG CTGACATGCT 550
CAGAACAAGA TGGTTCCCCA CCTTCTGAAT ACACCTGGTT CAAAGATGGG 600
ATAGTGATGC CTACGAATCC CAAAAGCACC CGTGCCTTCA GCAACTCTTC 650
CTATGTCCTG AATCCCACAA CAGGAGAGCT GGTCTTTGAT CCCCTGTCAG 700
CCTCTGATAC TGGAGAATAC AGCTGT 726
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FIG._4B

consen02 SEQ ID NO:5

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GCAGGCAAAG TACCAGGGCC GCCTGCATGT GAGCCACAAG GTTCCAGGAG 50
ATGTATCCCT CCAATTGAGC ACCCTGGAGA TGGATGACCG GAGCCACTAC 100
ACGTGTGAAG TCACCTGGCA GACTCCTGAT GGCAACCAAG TCGTGAGAGA 150
TAAGATTACT GAGCTCCGTG TCCAGAAACT CTCTGTCTCC AAGCCCACAG 200
TGACAACTGG CAGCGGTTAT GGCTTCACGG TGCCCCAGGG AATGAGGATT 250
AGCCTTCAAT GCCAGGGTTC GGGGTTCTCC TCCCATCAGT TATATTTGGT 300
ATAAGCAACA GACTAATAAC CAGGGAACCC ATCAAAGTAG CAACCCTAAG 350
TACCTTACTC TTCAAGCCTG CGGTGATAGC CGACTCAGGC TCCTATTTCT 400
GCACTGCCAA GGGCCAGGTT GGCTCTGAGC AGCACAGCGA CATTGTGAAG 450
TTTGTGGTCA AAGACTCCTC AAAGCTACTC AAGACCAAGA CTGAGGCACC 500
TACAACCATG ACATACCCCT TGAAAGCAAC ATCTACAGTG AAGCAGTCCT 550
GGGACTGGAC CACTGACATG GATGGCTACC TTGGAGAGAC CAGTGCTGGG 600
CCAGGAAAGA GCCTGCCTGT CTTTGCCATC ATCCTCATCA TCTCCTTGTG 650
CTGTATGGTG GTTTTTACCA TGGCCTATAT CATGCTCTGT CGGAAGACAT 700
CCCAACAAGA GCATGTCTAC GAAGCAGCCA GGGCACATGC CAGAGAGGCC 750
AACGACTCTG GAGAAACCAT GAGGGTGGCC ATCTTCGCAA GTGGCTGCTC 800
CAGTGATGAG CCAACTTCCC AGAATCTGGG GCAACAACTA CTCTGATGAG 850
CCCTGCATAG GACAGGAGTA CCAGATCATC GCCCAGATCA ATGGCAACTA 900
CGCCCGCCTG CTGGACACAG TTCCTCTGGA TTATGAGTTT CTGGCCACTG 950
AGGGCAAAAG TGTCTGTTAA AAATGCCCCA TTAGGCCAGG ATCTGCTGAC 1000
ATAATTGCCT AGTCAGTCCT TGCCTTCTGC ATGGCCTTCT TCCCTGCTAC 1050
CTCTCTTCCT GGATAGCCCA AAGTGTCCGC CTACCAACAC TGGAGCCGCT 1100
GGGAGTCACT GGCTTTGCCC TGGAATTTGC CAGATGCATC TCAAGTAAGC 1150
CAGCTGCTGG ATTTGGCTCT GGGCCCTTCT AGTATCTCTG CCGGGGGCTT 1200
CTGGTACTCC TCTCTAAATA CCAGAGGGAA GATGCCCATA GCACTAGGAC 1250
TTGGTCATCA TGCCTACAGA CACTATTCAA CTTTGGCATC TTGCCACCAG 1300
AAGACCCGAG GGGAGGCTCA GCTCTGCCAG CTCAGAGGAC CAGCTATATC 1350
CAGGATCATT TCTCTTTCTT CAGGGCCAGA CAGCTTTTAA TTGAAATTGT 1400
TATTTCACAG GCCAGGGTTC AGTTCTGCTC CTCCACTATA AGTCTAATGT 1450
TCTGACTCTC TCCTGGTGCT CAATAAATAT CTAATCATAA CAGCAAAAAA 1500
AAA 1503
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FIG._4C

SEQ ID NO:11 GGAGTCCTT CGGCGGCTGT TGTGTCAGTG GCCTGATCGC GATGGGGACA AAGGCGCAAG TCGAGAGGAA ACTGTTGTGC CTCTTCATAT 100
TGGCGATCCT GTTGTGCTCC CTGGCATTGG GCAGTGTTAC AGTGCACTCT TCTGAACCTG AAGTCAGAAT TCCTGAGAAT AATCCTGTGA AGTTGTCCTG 200
TGCCTACTCG GGCTTTTCTT CTCCCCGTGT GGAGTGGAAG TTTGACCAAG GAGACACCAC CAGACTCGTT TGCTATAATA ACAAGATCAC AGCTTCCTAT 300
GAGGACCGGG TGACCTTCTT GCCAACTGGT ATCACCTTCA AGTCCGTGAC ACGGGAAGAC ACTGGGACAT ACACTTGTAT GGTCTCTGAG GAAGGCGGCA 400
ACAGCTATGG GGAGGTCAAG GTCAAGCTCA TCGTGCTTGT GCCTCCATCC AAGCCTACAG TTAACATCCC CTCCTCTGCC ACCATTGGGA ACCGGGCAGT 500
GCTGACATGC TCAGAACAAG ATGGTTCCCC ACCTTCTGAA TACACCTGGT TCAAAGATGG GATAGTGATG CCTACGAATC CCAAAAGCAC CCGTGCCTTC 600
AGCAACTCTT CCTATGTCCT GAATCCCACA ACAGGAGAGC TGGTCTTTGA TCCCCTGTCA GCCTCTGATA CTGGAGAATA CAGCTGTGAG GCACGGAATG 700
GGTATGGGAC ACCCATGACT TCAAATGCTG TGCGCATGGA AGCTGTGGAG CGGAATGTGG GGGTCATCGT GGCAGCCGTC CTTGTAACCC TGATTCTCCT 800
GGGAATCTTG GTTTTTGGCA TCTGGTTTGC CTATAGCCGA GGCCACTTTG ACAGAACAAA GAAAGGGACT TCGAGTAAGA AGGTGATTTA CAGCCAGCCT 900
AGTGCCCGAA GTGAAGGAGA ATTCAAACAG ACCTCGTCAT TCCTGGTGTG AGCCTGGTCG GCTCACCGCC TATCATCTGC ATTTGCCTTA CTCAGGTGCT 1000
ACCGGACTCT GGCCCCTGAT GTCTGTAGTT TCACAGGATG CCTTATTTGT CTTCTACACC CCACAGGGCC CCCTACTTCT TCGGATGTGT TTTTAATAAT 1100
GTCAGCTATG TGCCCCATCC TCCTTCATGC CCTCCCTCCC TTTCCTACCA CTGCTGAGTG GCCTGGAACT TGTTTAAAGT GTTTATTCCC CATTTCTTTG 1200
AGGGATCAGG AAGGAATCCT GGGTATGCCA TTGACTTCCC TTCTAAGTAG ACAGCAAAAA TGGCGGGGGT CGCAGGAATC TGCACTCAAC TGCCCACCTG 1300
GCTGGCAGGG ATCTTTGAAT AGGTATCTTG AGCTTGGTTC TGGGCTCTTT CCTTGTGTAC TGACGACCAG GGCCAGCTGT TCTAGAGCGG GAATTAGAGG 1400
CTAGAGCGGC TGAAATGGTT GTTTGGTGAT GACACTGGGG TCCTTCCATC TCTGGGGCCC ACTCTCTTCT GTCTTCCCAT GGGAAGTGCC ACTGGGATCC 1500
CTCTGCCCTG TCCTCCTGAA TACAAGCTGA CTGACATTGA CTGTGTCTGT GGAAAATGGG AGCTCTTGTT GTGGAGAGCA TAGTAAATTT TCAGAGAACT 1600
TGAAGCCAAA AGGATTTAAA ACCGCTGCTC TAAAGAAAAG AAAACTGGAG GCTGGGCGCA GTGGCTCACG CCTGTAATCC CAGAGGCTGA GGCAGGCGGA 1700
TCACCTGAGG TCGGGAGTTC GGGATCAGCC TGACCAACAT GGAGAAACCC TACTGGAAAT ACAAAGTTAG CCAGGCATGG TGGTGCATGC CTGTAGTCCC 1800
AGCTGCTCAG GAGCCTGGCA ACAAGAGCAA AACTCCAGCT CA 1842

FIG._5

SEQ ID NO:7

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  1 CCCACGCGTC CGCCCACGCG TCCGCCCACG GGTCCGCCCA CGCGTCCGGG CCACCAGAAG TTTGAGCCTC TTTGGTAGCA GGAGGCTGGA AGAAAGGACA
    GGGTGCGCAG GCGGGTGCGC AGGCGGGTGC CCAGGCGGGT GCGCAGGCCC GGTGGTCTTC AAACTCGGAG AAACCATCGT CCTCCGACCT TCTTTCCTGT

101 GAAGTAGCTC TGGCTGTGAT GGGGATCTTA CTGGGCCTGC TACTCCTGGG GCACCTAACA GTGGACACTT ATGGCCGTCC CATCCTGGAA GTGCCAGAGA
    CTTCATCGAG ACCGACACTA CCCCTAGAAT GACCCGGACG ATGAGGACCC CGTGGATTGT CACCTGTGAA TACCGGCAGG GTAGGACCTT CACGGTCTCT
  1         SEQ ID NO:2 M  G  I  L  L  G  L  L  L  L  G  H  L  T  V  D  T  Y  G  R  P  I  L  E  V  P  E  S
                        ^MET

201 GTGTAACAGG ACCTTGGAAA GGGGATGTGA ATCTTCCCTG CACCTATGAC CCCCTGCAAG GCTACACCCA AGTCTTGGTG AAGTGGCTGG TACAACGTGG
    CACATTGTCC TGGAACCTTT CCCCTACACT TAGAAGGGAC GTGGATACTG GGGGACGTTC CGATGTGGGT TCAGAACCAC TTCACCGACC ATGTTGCACC
 29  V  T  G  P  W  K  G  D  V  N  L  P  C  T  Y  D  P  L  Q  G  Y  T  Q  V  L  V  K  W  L  V  Q  R  G

301 CTCAGACCCT GTCACCATCT TTCTACGTGA CTCTTCTGGA GACCATATCC AGCAGGCAAA GTACCAGGGC CGCCTGCATG TGAGCCACAA GGTTCCAGGA
    GAGTCTGGGA CAGTGGTAGA AAGATGCACT GAGAAGACCT CTGGTATAGG TCGTCCGTTT CATGGTCCCG GCGGACGTAC ACTCGGTGTT CCAAGGTCCT
 62  S  D  P  V  T  I  F  L  R  D  S  S  G  D  H  I  Q  Q  A  K  Y  Q  G  R  L  H  V  S  H  K  V  P  G

401 GATGTATCCC TCCAATTGAG CACCCTGGAG ATGGATGACC GGAGCCACTA CACGTGTGAA GTCACCTGGC AGACTCCTGA TGGCAACCAA GTCGTGAGAG
    CTACATAGGG AGGTTAACTC GTGGGACCTC TACCTACTGG CCTCGGTGAT GTGCACACTT CAGTGGACCG TCTGAGGACT ACCGTTGGTT CAGCACTCTC
 95 D  V  S  L  Q  L  S  T  L  E  M  D  D  R  S  H  Y  T  C  E  V  T  W  Q  T  P  D  G  N  Q  V  V  R  D

501 ATAAGATTAC TGAGCTCCGT GTCCAGAAAC TCTCTGTCTC CAAGCCCACA GTGACAACTG GCAGCGGTTA TGGCTTCACG GTGCCCCAGG GAATGAGGAT
    TATTCTAATG ACTCGAGGCA CAGGTCTTTG AGAGACAGAG GTTCGGGTGT CACTGTTGAC CGTCGCCAAT ACCGAAGTGC CACGGGGTCC CTTACTCCTA
129  K  I  T  E  L  R  V  Q  K  L  S  V  S  K  P  T  V  T  T  G  S  G  Y  G  F  T  V  P  Q  G  M  R  I

601 TAGCCTTCAA TGCCAGGCTC GGGGTTCTCC TCCCATCAGT TATATTTGGT ATAAGCAACA GACTAATAAC CAGGAACCCA TCAAAGTAGC AACCCTAAGT
    ATCGGAAGTT ACGGTCCGAG CCCCAAGAGG AGGGTAGTCA ATATAAACCA TATTCGTTGT CTGATTATTG GTCCTTGGGT AGTTTCATCG TTGGGATTCA
162  S  L  Q  C  Q  A  R  G  S  P  P  I  S  Y  I  W  Y  K  Q  Q  T  N  N  Q  E  P  I  K  V  A  T  L  S
```

FIG._6A

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SEQ ID NO:7  701 ACCTTACTCT TCAAGCCTGC GGTGATAGCC GACTCAGGCT CCTATTTCTG CACTGCCAAG GGCCAGGTTG GCTCTGAGCA GCACAGCGAC ATTGTGAAGT
                 TGGAATGAGA AGTTCGGACG CCACTATCGG CTGAGTCCGA GGATAAAGAC GTGACGGTTC CCGGTCCAAC CGAGACTCGT CGTGTCGCTG TAACACTTCA
SEQ ID NO:2  195 T  L  L  F   K  P  A   V  I  A   D  S  G  S   Y  F  C   T  A  K   G  Q  V  G   S  E  Q   H  S  D   I  V  K  F

                 801 TTGTGGTCAA AGACTCCTCA AAGCTACTCA AGACCAAGAC TGAGGCACCT ACAACCATGA CATACCCCTT GAAAGCAACA TCTACAGTGA AGCAGTCCTG
                     AACACCAGTT TCTGAGGAGT TTCGATGAGT TCTGGTTCTG ACTCCGTGGA TGTTGGTACT GTATGGGGAA CTTTCGTTGT AGATGTCACT TCGTCAGGAC
                 229   V  V  K   D  S  S   K  L  L  K   T  K  T   E  A  P   T  T  M  T   Y  P  L   K  A  T   S  T  V  K   Q  S  W

                 901 GGACTGGACC ACTGACATGG ATGGCTACCT TGGAGAGACC AGTGCTGGGC CAGGAAAGAG CCTGCCTGTC TTTGCCATCA TCCTCATCAT CTCCTTGTGC
                     CCTGACCTGG TGACTGTACC TACCGATGGA ACCTCTCTGG TCACGACCCG GTCCTTTCTC GGACGGACAG AAACGGTAGT AGGAGTAGTA GAGGAACACG
                 262   D  W  T   T  D  M  D   G  Y  L   G  E  T   S  A  G  P   G  K  S   L  P  V   F  A  I  I   L  I  I   S  L  C

                1001 TGTATGGTGG TTTTTACCAT GGCCTATATC ATGCTCTGTC GGAAGACATC CCAACAAGAG CATGTCTACG AAGCAGCCAG GTAAGAAAGT CTCTCCTCTT
                     ACATACCACC AAAAATGGTA CCGGATATAG TACGAGACAG CCTTCTGTAG GGTTGTTCTC GTACAGATGC TTCGTCGGTC CATTCTTTCA GAGAGGAGAA
                 295 C  M  V  V   F  T  M   A  Y  I   M  L  C  R   K  T  S   Q  Q  E   H  V  Y  E   A  A  R   O

                1101 CCATTTTTGA CCCCGTCCCT GCCCTCAATT TTGATTACTG GCAGGAAATG TGGAGGAAGG GGGGTGTGGC ACAGACCCAA TCCTAAGGCC GGAGGCCTTC
                     GGTAAAAAACT GGGGCAGGGA CGGGAGTTAA AACTAATGAC CGTCCTTTAC ACCTCCTTCC CCCCACACCG TGTCTGGGTT AGGATTCCGG CCTCCGGAAG

                1201 AGGGTCAGGA CATAGCTGCC TTCCCTCTCT CAGGCACCTT CTGAGGTTGT TTTGGCCCTC TGAACACAAA GGATAATTTA GATCCATCTG CCTTCTGCTT
                     TCCCAGTCCT GTATCGACGG AAGGGAGAGA GTCCGTGGAA GACTCCAACA AAACCGGGAG ACTTGTGTTT CCTATTAAAT CTAGGTAGAC GGAAGACGAA

                1301 CCAGAATCCC TGGGTGGTAG GATCCTGATA ATTAATTGGC AAGAATTGAG GCAGAAGGGT GGGAAACCAG GACCACAGCC CCAAGTCCCT TCTTATGGGT
                     GGTCTTAGGG ACCCACCATC CTAGGACTAT TAATTAACCG TTCTTAACTC CGTCTTCCCA CCCTTTGGTC CTGGTGTCGG GGTTCAGGGA AGAATACCCA

                1401 GGTGGGCTCT TGGGCCATAG GGCACATGCC AGAGAGGCCA ACGACTCTGG AGAAACCATG AGGGTGGCCA TCTTCGCAAG TGGCTGCTCC AGTGATGAGC
                     CCACCCGAGA ACCCGGTATC CCGTGTACGG TCTCTCCGGT TGCTGAGACC TCTTTGGTAC TCCCACCGGT AGAAGCGTTC ACCGACGAGG TCACTACTCG

                1501 CAACTTCCCA GAATCTGGGC AACAACTACT CTGATGAGCC CTGCATAGGA CAGGAGTACC AGATCATCGC CCAGATCAAT GGCAACTACG CCCGCCTGCT
                     GTTGAAGGGT CTTAGACCCG TTGTTGATGA GACTACTCGG GACGTATCCT GTCCTCATGG TCTAGTAGCG GGTCTAGTTA CCGTTGATGC GGGCGGACGA
```

FIG._6B

SEQ ID NO:7

```
1601 GGACACAGTT CCTCTGGATT ATGAGTTTCT GGCCACTGAG GGCAAAAGTG TCTGTTAAAA ATGCCCCATT AGGCCAGGAT CTGCTGACAT AATTGCCTAG
     CCTGTGTCAA GGAGACCTAA TACTCAAAGA CCGGTGACTC CCGTTTTCAC AGACAATTTT TACGGGGTAA TCCGGTCCTA GACGACTGTA TTAACGGATC

1701 TCAGTCCTTG CCTTCTGCAT GGCCTTCTTC CCTGCTACCT CTCTTCCTGG ATAGCCCAAA GTGTCCGCCT ACCAACACTG GAGCCGCTGG GAGTCACTGG
     AGTCAGGAAC GGAAGACGTA CCGGAAGAAG GGACGATGGA GAGAAGGACC TATCGGGTTT CACAGGCGGA TGGTTGTGAC CTCGGCGACC CTCAGTGACC

1801 CTTTGCCCTG GAATTTGCCA GATGCATCTC AAGTAAGCCA GCTGCTGGAT TTGGCTCTGG GCCCTTCTAG TATCTCTGCC GGGGGCTTCT GGTACTCCTC
     GAAACGGGAC CTTAAACGGT CTACGTAGAG TTCATTCGGT CGACGACCTA AACCGAGACC CGGGAAGATC ATAGAGACGG CCCCCGAAGA CCATGAGGAG

1901 TCTAAATACC AGAGGGAAGA TGCCCATAGC ACTAGGACTT GGTCATCATG CCTACAGACA CTATTCAACT TTGGCATCTT GCCACCAGAA GACCCGAGGG
     AGATTTATGG TCTCCCTTCT ACGGGTATCG TGATCCTGAA CCAGTAGTAC GGATGTCTGT GATAAGTTGA AACCGTAGAA CGGTGGTCTT CTGGGCTCCC

2001 AGGCTCAGCT CTGCCAGCTC AGAGGACCAG CTATATCCAG GATCATTTCT CTTTCTTCAG GGCCAGACAG CTTTTAATTG AAATTGTTAT TTCACAGGCC
     TCCGAGTCGA GACGGTCGAG TCTCCTGGTC GATATAGGTC CTAGTAAAGA GAAAGAAGTC CCGGTCTGTC CAAAATTAAC TTTAACAATA AAGTGTCCGG

2101 AGGGTTCAGT TCTGCTCCTC CACTATAAGT CTAATGTTCT GACTCTCTCC TGGTGCTCAA TAAATATCTA ATCATAACAG C
     TCCCAAGTCA AGACGAGGAG GTGATATTCA GATTACAAGA CTGAGAGAGG ACCACGAGTT ATTTATAGAT TAGTATTGTC G
```

FIG._6C

SEQ ID NO:8

CCCAGAAGTTCAAGGGCCCCCGGCCTCCTGCGCTCCTGCCGCCGGGACCCTCGACCTCCT
CAGAGCAGCCGGCTGCCGCCCCGGGAAGATGGCGAGCAGGAGCCGCCACCGCCTCCTCCT
GCTGCTGCTGCGCTACCTGGTGGTCGCCCTGGGCTATCATAAGGCCTATGGGTTTTCTGC
CCCAAAAGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTTAGCCTGCAA
AACCCCAAAGAAGACTGTTTCCTCCAGATTAGAGTGGAAGAAACTGGGTCGGAGTGTCTC
CTTTGTCTACTATCAACAGACTCTTCAAGGTGATTTTAAAAATCGAGCTGAGATGATAGA
TTTCAATATCCGGATCAAAAATGTGACAAGAAGTGATGCGGGGAAATATCGTTGTGAAGT
TAGTGCCCCATCTGAGCAAGGCCAAAACCTGGAAGAGGATACAGTCACTCTGGAAGTATT
AGTGGCTCCAGCAGTTCCATCATGTGAAGTACCCTCTTCTGCTCTGAGTGGAACTGTGGT
AGAGCTACGATGTCAAGACAAAGAAGGGAATCCAGCTCCTGAATACACATGGTTTAAGGA
TGGCATCCGTTTGCTAGAAAATCCCAGACTTGGCTCCCAAAGCACCAACAGCTCATACAC
AATGAATACAAAAACTGGAACTCTGCAATTTAATACTGTTTCCAAACTGGACACTGGAGA
ATATTCCTGTGAAGCCCGCAATTCTGTTGGATATCGCAGGTGTCCTGGGAAACGAATGCA
AGTAGATGATCTCAACATAAGTGGCATCATAGCAGCCGTAGTAGTTGTGGCCTTAGTGAT
TTCCGTTTGTGGCCTTGGTGTATGCTATGCTCAGAGGAAAGGCTACTTTTCAAAAGAAAC
CTCCTTCCAGAAGAGTAATTCTTCATCTAAAGCCACGACAATGAGTGAAAATGTGCAGTG
GCTCACGCCTGTAATCCCAGCACTTTGGAAGGCCGCGGCGGGCGGATCACGAGGTCAGGA
GTTCTAGACCAGTCTGGCCAATATGGTGAAACCCCATCTCTACTAAAATACAAAAATTAG
CTGGGCATGGTGGCATGTGCCTGCAGTTCCAGCTGCTTGGGAGACAGGAGAATCACTTGA
ACCCGGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGCCACTGCAGTCCAGCCTGGGTAA
CAGAGCAAGATTCCATCTCAAAAAATAAAATAAATAAATAAATAAATACTGGTTTTTACC
TGTAGAATTCTTACAATAAATATAGCTTGATATTC

FIG._7

SEQ ID NO:9

MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTVSSR
LEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQN
LEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPR
LGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGI
IAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENVQWLTPVIPALW
KAAAGGSRGQEF

FIG._11

SEQ ID NO:5

```
  1 GCAGGCAAAG TACCAGGGCC GCCTGCATGT GAGCCACAAG GTTCCAGGAG ATGTATCCCT CCAATTGAGC ACCCTGGAGA TGGATGACCG GAGCCACTAC
    CGTCCGTTTC ATGGTCCCGG CGGACGTACA CTCGGTGTTC CAAGGTCCTC TACATAGGGA GGTTAACTCG TGGGACCTCT ACCTACTGGC CTCGGTGATG
                                                                ^42257.f1 SEQ ID NO:18          ^42257.p1 SEQ ID NO:22

101 ACGTGTGAAG TCACCTGGCA GACTCCTGAT GGCAACCAAG TCGTGAGAGA TAAGATTACT GAGCTCCGTG TCCAGAAACT CTCTGTCTCC AAGCCCACAG
    TGCACACTTC AGTGGACCGT CTGAGGACTA CCGTTGGTTC AGCACTCTCT ATTCTAATGA CTCGAGGCAC AGGTCTTTGA GAGACAGAGG TTCGGGTGTC

201 TGACAACTGG CAGCGGTTAT GGCTTCACGG TGCCCCAGGG AATGAGGATT AGCCTTCAAT GCCAGGGTTC GGGGTTCTCC TCCCATCAGT TATATTTGGT
    ACTGTTGACC GTCGCCAATA CCGAAGTGCC ACGGGGTCCC TTACTCCTAA TCGGAAGTTA CGGTCCCAAG CCCCAAGAGG AGGGTAGTCA ATATAAACCA

301 ATAAGCAACA GACTAATAAC CAGGGAACCC ATCAAAGTAG CAACCCTAAG TACCTTACTC TTCAAGCCTG CGGTGATAGC CGACTCAGGC TCCTATTTCT
    TATTCGTTGT CTGATTATTG GTCCCTTGGG TAGTTTCATC GTTGGGATTC ATGGAATGAG AAGTTCGGAC GCCACTATCG GCTGAGTCCG AGGATAAAGA

401 GCACTGCCAA GGGCCAGGTT GGCTCTGAGC AGCACAGCGA CATTGTGAAG TTTGTGGTCA AAGACTCCTC AAAGCTACTC AAGACCAAGA CTGAGGCACC
    CGTGACGGTT CCCGGTCCAA CCGAGACTCG TCGTGTCGCT GTAACACTTC AAACACCAGT TTCTGAGGAG TTTCGATGAG TTCTGGTTCT GACTCCGTGG
                                                ^42257.r1 SEQ ID NO:20

501 TACAACCATG ACATACCCCT TGAAAGCAAC ATCTACAGTG AAGCAGTCCT GGGACTGGAC CACTGACATG GATGGCTACC TTGGAGAGAC CAGTGCTGGG
    ATGTTGGTAC TGTATGGGGA ACTTTCGTTG TAGATGTCAC TTCGTCAGGA CCCTGACCTG GTGACTGTAC CTACCGATGG AACCTCTCTG GTCACGACCC

601 CCAGGAAAGA GCCTGCCTGT CTTTGCCATC ATCCTCATCA TCTCCTTGTG CTGTATGGTG GTTTTTACCA TGGCCTATAT CATGCTCTGT CGGAAGACAT
    GGTCCTTTCT CGGACGGACA GAAACGGTAG TAGGAGTAGT AGAGGAACAC GACATACCAC CAAAAATGGT ACCGGATATA GTACGAGACA GCCTTCTGTA
                                                                                    ^42257.f2 SEQ ID NO:19

701 CCCAACAAGA GCATGTCTAC GAAGCAGCCA GGGCACATGC CAGAGAGGCC AACGACTCTG GAGAAACCAT GAGGGTGGCC ATCTTCGCAA GTGGCTGCTC
    GGGTTGTTCT CGTACAGATG CTTCGTCGGT CCCGTGTACG GTCTCTCCGG TTGCTGAGAC CTCTTTGGTA CTCCCACCGG TAGAAGCGTT CACCGACGAG
```

FIG._9A

SEQ ID NO:5

```
 801 CAGTGATGAG CCAACTTCCC AGAATCTGGG GCAACAACTA CTCTGATGAG CCCTGCATAG GACAGGAGTA CCAGATCATC GCCCAGATCA ATGGCAACTA
     GTCACTACTC GGTTGAAGGG TCTTAGACCC CGTTGTTGAT GAGACTACTC GGGACGTATC CTGTCCTCAT GGTCTAGTAG CGGGTCTAGT TACCGTTGAT

 901 CGCCCGCCTG CTGGACACAG TTCCTCTGGA TTATGAGTTT CTGGCCACTG AGGGCAAAAG TGTCTGTTAA AAATGCCCCA TTAGGCCAGG ATCTGCTGAC
     GCGGGCGGAC GACCTGTGTC AAGGAGACCT AATACTCAAA GACCGGTGAC TCCCGTTTTC ACAGACAATT TTTACGGGGT AATCCGGTCC TAGACGACTG

1001 ATAATTGCCT AGTCAGTCCT TGCCTTCTGC ATGGCCTTCT TCCCTGCTAC CTCTCTTCCT GGATAGCCCA AAGTGTCCGC CTACCAACAC TGGAGCCGCT
     TATTAACGGA TCAGTCAGGA ACGGAAGACG TACCGGAAGA AGGGACGATG GAGAGAAGGA CCTATCGGGT TTCACAGGCG GATGGTTGTG ACCTCGGCGA

1101 GGGAGTCACT GGCTTTGCCC TGGAATTTGC CAGATGCATC TCAAGTAAGC CAGCTGCTGG ATTTGGCTCT GGGCCCTTCT AGTATCTCTG CCGGGGGCTT
     CCCTCAGTGA CCGAAACGGG ACCTTAAACG GTCTACGTAG AGTTCATTCG GTCGACGACC TAAACCGAGA CCCGGGAAGA TCATAGAGAC GGCCCCCGAA
                                                                                  ^42257.r2 SEQ ID NO:21

1201 CTGGTACTCC TCTCTAAATA CCAGAGGGAA GATGCCCATA GCACTAGGAC TTGGTCATCA TGCCTACAGA CACTATTCAA CTTTGGCATC TTGCCACCAG
     GACCATGAGG AGAGATTTAT GGTCTCCCTT CTACGGGTAT CGTGATCCTG AACCAGTAGT ACGGATGTCT GTGATAAGTT GAAACCGTAG AACGGTGGTC

1301 AAGACCCGAG GGGAGGCTCA GCTCTGCCAG CTCAGAGGAC CAGCTATATC CAGGATCATT TCTCTTTCTT CAGGGCCAGA CAGCTTTTAA TTGAAATTGT
     TTCTGGGCTC CCCTCCGAGT CGAGACGGTC GAGTCTCCTG GTCGATATAG GTCCTAGTAA AGAGAAAGAA GTCCCGGTCT GTCGAAAATT AACTTTAACA

1401 TATTTCACAG GCCAGGGTTC AGTTCTGCTC CTCCACTATA AGTCTAATGT TCTGACTCTC TCCTGGTGCT CAATAAATAT CTAATCATAA CAGCAAAAAA
     ATAAAGTGTC CGGTCCCAAG TCAAGACGAG GAGGTGATAT TCAGATTACA AGACTGAGAG AGGACCACGA GTTATTTATA GATTAGTATT GTCGTTTTTT

1501 AAA
     TTT
```

FIG._9B

		FRAME	SCORE	MATCH	PCT
A33_HUMAN	A33 ANTIGEN PRECURSOR - HOMO SAPIENS	+1	246	81	30

A33_HUMAN - A33 ANTIGEN PRECURSOR - HOMO SAPIENS (319 aa)
SCORE = 246 (86.6 BITS), EXPECT = 2.8e-19, P = 2.8e-19
IDENTITIES = 81/268 (30%), POSITIVES = 131/268 (48%), AT 121,17, FRAME = +1

```
DNA40628  121 LALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPR---VEW-KFDQGDTTRLVC--YNN
SEQ ID NO:23
              . . ...* . .  .*  .   * * * *   .* *   ..* *     * *.*   ..*
A33_human  17 VTVDAISVETPQDVLRASQGKSVTLPCTYHTSTSSREGLIQWDKLLLTHTERVVIWPFSN
SEQ ID NO:24

DNA40628  283 K--ITAS-YEDRVTFL------PTGITFKSVTREDTGTYTCMVS---EEGGNSYGEVKVK
              *  *    *..**.          **   .*  * *** * **   .  **.  . .*.
A33_human  77 KNYIHGELYKNRVSISNNAEQSDASITIDQLTMADNGTYECSVSLMSDLEGNT--KSRVR

DNA40628  427 LIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKSTRAFSN
              *.********   *     ***   ***  ..***  .*.* .  *.    *
A33_human 135 LLVLVPPSKPECGIEGETIIGNNIQLTCQSKEGSPTPQYSWKRYNILNQEQP--------

DNA40628  607 SSYVLNPTTGELV-FDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGV---IVA
                . * .*. *    .*   .* * * . * **   .  * . .   ** .   *
A33_human 187 ---LAQPASGQPVSLKNISTDTSGYYICTSSNEEGTQFCNITVAVRSPSMNVALYVGIAV

DNA40628  775 AVLVTLILLGILVFGIWFAYSRGHFDRT--KKGTSSKKVIYSQP
               *.  **..**...       **  * *  *.     .  * .*
A33_human 244 GVVAALIIIGIIIY---CCCCRGKDDNTEDKEDARPNREAYEEP
```

FIG._10A

SCORE = 245 (86.2 BITS), EXPECT =3.6e-19, P = 3.6e-19
IDENTITIES = 83/273 (30%), POSITIVES = 131/273 (47%), AT 112,12, FRAME = +1

```
DNA40628   112 LCSL--ALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPR---VEW-KFDQGDTTRLVC
SEQ ID NO:25
               **..   . ...* . .  .*  .   * * * *   .* *   ..* *     * *.*
A33 human   12 LCAVRVTVDAISVETPQDVLRASQGKSVTLPCTYHTSTSSREGLIQWDKLLLTHTERVVI
SEQ ID NO:26

DNA40628   274 --YNNK--ITAS-YEDRVTFL------PTGITFKSVTREDTGTYTCMVSEEGGNSYGEVK
                 ..**  *    *..**.           **   .*  * *** * **    .  *  *
A33_human   72 WPFSNKNYIHGELYKNRVSISNNAEQSDASITIDQLTMADNGTYECSVSLMS-DLEGNTK

DNA40628   421 --VKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKSTR
                 *.*.********   *     ***   ***  ..***  .*.* .  *.    *
A33_human  131 SRVRLLVLVPPSKPECGIEGETIIGNNIQLTCQSKEGSPTPQYSWKRYNILNQEQP----

DNA40628   595 AFSNSSYVLNPTTGELV-FDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGV--
                     . * .*. *    .*   .* * * . *  **   .  * . .   ** .
A33_human  187 -------LAQPASGQPVSLKNISTDTSGYYICTSSNEEGTQFCNITVAVRSPSMNVALYV

DNA40628   766 -IVAAVLVTLILLGILVFGIWFAYSRGHFDRT--KKGTSSKKVIYSQP
                *   *.  **..**...       **  * *  *.     .  * .*
A33_human  240 GIAVGVVAALIIIGIIIY---CCCCRGKDDNTEDKEDARPNREAYEEP
```

FIG._10B

```
SEQ ID NO: 6  A33_hum    1 ........MVGKMWPVLWTLCAVRVTVDAISVETPQDVLRASQGKSVTL
SEQ ID NO: 1  40628      1 MGTKAQVERKLLCLFILAILLCS..LALGSVTVHSSEPEVRIPENNPVKL

              A33_hum   42 PCTYHTSTSSREGLIQWDKLLLTHTERVVIWPFSNKNYIHGELYKNRVSI
              40628     49 SCAYSGFSSPR...VEW.KFDQGDTTRLVC..YNNK..ITAS.YEDRVTF

              A33_hum   92 SNNAEQSDASITIDQLTMADNGTYECSVSLMSDLEGNTKSRVRLLVLVPP
              40628     90 ......LPTGITFKSVTREDTGTYTCMVSEEGG.NSYGEVKVKLIVLVPP

              A33_hum  142 SKPECGIEGETIIGNNIQLTCQSKEGSPTPQYSWKRYNILNQEQP.....
              40628    133 SKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKSTRA

              A33_hum  187 ......LAQPASGQPVSLKNISTDTSGYYICTSSNEEGTQFCNITVAVRS
              40628    183 FSNSSYVLNPTTGE.LVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEA

              A33_hum  231 PSMNVALYVGIAVGVVAALIIIGIIIYCC.CCRGKDDNTEDKEDARPNRE
              40628    232 VERNVGV...IVAAVLVTLILLGILVFGIWFAYSRGHFDRTKKGTSSKKV

              A33_hum  280 AYEEPPEQLRELSRERFEEDDYRQEEQRSTGRESPDHLDQ
              40628    279 IYSQPSARSEGEFKQTSSFLV
```

FIG._12

```
SEQ ID NO: 6  A33_hum    1 MVGKMWPVLWTLCAVRVTVDAISVETPQDVLRASQGKSVTLPCTYHTSTS
SEQ ID NO: 2  45416      1 .MGILLGLLLLGHLTVDTYGRPILEVPESVTGPWKG.DVNLPCTYDPLQG

              A33_hum   51 SREGLIQWDKLLLTHTERVVIW.PFSNKNYIHGELYKNRVSISNNAEQSD
              45416     49 YTQVLVKW..LVQRGSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKV.PGD

              A33_hum  100 ASITIDQLTMADNGTYECSVS.LMSDLEGNTKSRV.....RLLVLVPPS
              45416     96 VSLQLSTLEMDDRSHYTCEVTWQTPDGNQVVRDKITELRVQKLSVSKPTV

              A33_hum  143 KPECGIEGETIIGNNIQLTCQSKEGSPTPQYSWKRYNILNQEQPLAQPAS
              45416    146 TTGSGYGFTVPQGMRISLQCQAR.GSPPISYIW..YKQQTNNQEPIKVAT

              A33_hum  193 GQPVSLKNISTDTSGYYICTSSNEEGT.QFCNI.TVAVRSPSMNVALYVG
              45416    193 LSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTKTE

              A33_hum  241 IAVGVVAALIIIGIIIYCCCCRGKDDNTEDKEDARPNREAYEEPPEQLRE
              45416    243 APTTMTYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIILIIS

              A33_hum  291 LSRERERERDDYRQEEQRSTGRESPDHLDQ
              45416    293 LCCMVVFTMAYIMLCRKTSQQEHVYEAAR
```

FIG._13

```
SEQ ID NO: 6  A33_hum   1  ..MVGKMWPVLWTLCAVRVTVD.....AISVETPQDVLRASQGKSVTLPC
SEQ ID NO: 9  35638     1  MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILAC

              A33_hum  44  TYHTSTSSREGLIQWDKLLLTHTERVVIWPFSNKNYIHGELYKNRVSISN
              35638    51  ..KTPKKTVSSRLEWKKL.....GRSVSFVYYQQT.LQGD.FKNR.....

              A33_hum  94  NAEQSDASITIDQLTMADNGTYECSVSLMSDLEGN.TKSRVRLLVLVPPS
              35638    87  .AEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEEDTVTLEVLVAPA

              A33_hum 143  KPECGIEGETIIGNNIQLTCQSKEGSPTPQYSWKRYNILNQEQPLAQPAS
              35638   136  VPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQS

              A33_hum 193  GQPVSLKNISTDTSGYYICTSSNEEGTQFCNITVAV...RSPSMNVALYV
              35638   186  TNSSYTMNTKTGTLQFNT.VSKLDTGEYSCEARNSVGYRRCPGKRMQVDD

              A33_hum 240  GIAVGVVAALIIIGIIIYCC...CCRGKDDNTEDKEDARPNREAYEEPPE
              35638   235  LNISGIIAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATT

              A33_hum 287  QLRELSR.EREEEDDYRQEEQRSTGRESPDHLDQ
              35638   285  MSENVQWLTPVIPALWKAAAGGSRGQEF
```

FIG._14

```
SEQ ID NO: 10  jam      1 MGTEGKAGRKLLFLFT-SMILGSLVQGKGSVYTAQSDVQVPENESIKLTC
SEQ ID NO: 1   40628    1 MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSC

               jam     50 TYSGFSSPRVEWKFVQGSTTALVCYNSQITAPYADRVTFSSSGITFSSVT
               40628   51 AYSGFSSPRVEWKFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVT

               jam    100 RKDNGEYTCMVSEEGGQNYGEVSIHLTVLVPPSKPTISVPSSVTIGNRAV
               40628  101 REDTGTYTCMVSEEGGNSYGEVKVKLIVLVPPSKPTVNIPSSATIGNRAV

               jam    150 LTCSEHDGSPPSEYSWFKDGISMLTADAKKTRAFMNSSFTIDPKSGDLIF
               40628  151 LTCSEQDGSPPSEYTWFKDGI-VMPTNPKSTRAFSNSSYVLNPTTGELVF

               jam    200 DPVTAFDSGEYYCQAQNGYGTAMRSEAAHMDAVELNVGGIVAAVLVTLIL
               40628  200 DPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVAAVLVTLIL

               jam    250 LGLLIFGVWFAYSRGYFETTKKGTAPGKKVIYSQPSTRSEGEFKQTSSFL
               40628  250 LGILVFGIWFAYSRGHFDRTKKGT-SSKKVIYSQPSARSEGEFKQTSSFL

               jam    300 V
               40628  299 V
```

FIG._15

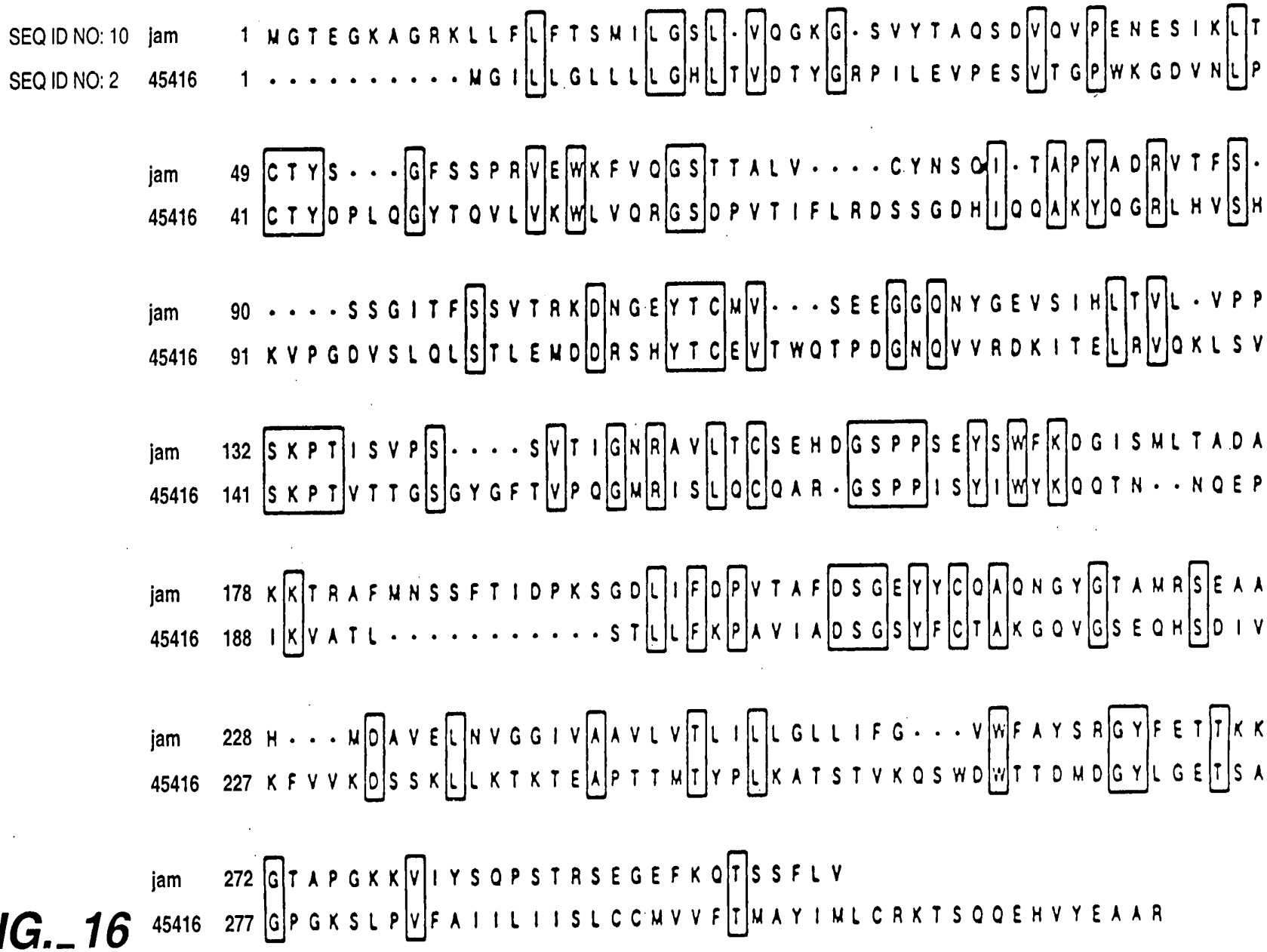
SEQ ID NO: 10 jam 1 MGTEGKAGRKLLFLFTSMILGSL·VQGKG·SVYTAQSDVQVPENESIKLT
SEQ ID NO: 2 45416 1 ··········MGILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLP
jam 49 CTYS···GFSSPRVEWKFVQGSTTALV····CYNSQI·TAPYADRVTFS·
45416 41 CTYDPLQGYTQVLVKWLVQRGSDPVTIFLRDSSGDHIQQAKYQGRLHVSH
jam 90 ····SSGITFSSVTRKDNGEYTCMV···SEEGGQNYGEVSIHLTVL·VPP
45416 91 KVPGDVSLQLSTLEMDDRSHYTCEVTWQTPDGNQVVRDKITELRVQKLSV
jam 132 SKPTISVPS····SVTIGNRAVLTCSEHDGSPPSEYSWFKDGISMLTADA
45416 141 SKPTVTTGSGYGFTVPQGMRISLQCQAR·GSPPISYIWYKQQTN··NQEP
jam 178 KKTRAFMNSSFTIDPKSGDLIFDPVTAFDSGEYYCQAQNGYGTAMRSEAA
45416 188 IKVATL··········STLLFKPAVIADSGSYFCTAKGQVGSEQHSDIV
jam 228 H···MDAVELNVGGIVAAVLVTLILLGLLIFG···VWFAYSRGYFETTKK
45416 227 KFVVKDSSKLLKTKTEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETSA
jam 272 GTAPGKKVIYSQPSTRSEGEFKQTSSFLV
45416 277 GPGKSLPVFAIILIISLCCMVVFTMAYIMLCRKTSQQEHVYEAAR

FIG._16

```
SEQ ID NO: 10  jam      1 MGTEGKAGRKLLFLFTSMILGSLVQGKGSVYTAQSDVQV...PENESIKL
SEQ ID NO: 29  35638    1 ..MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAIL

jam            48 TC.TYSGFSSPRVEWKFVQGSTTALVCYNSQITAPYADRVTFSSSGITFS
35638          49 ACKTPKKTVSSRLEWKKL.GRSVSFVYYQQTLQGDFKNRAEMIDFNIRIK

jam            97 SVTRKDNGEYTCMVS..EEGGQNYGEVSIHLTVLVPPSKPTISVPSSVTI
35638          98 NVTRSDAGKYRCEVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEVPSSALS

jam           145 GNRAVLTCSEHDGSPPSEYSWFKDGISMLTADAKKTRAFMNSSFTIDPKS
35638         148 GTVVELRCQDKEGNPAPEYTWFKDGIRLL.ENPRLGSQSTNSSYTMNTKT

jam           195 GDLIFDPVTAFDSGEYYCQAQNGYGTAMRSEAAHMDAVELNVGGIVAAVL
35638         197 GTLQFNTVSKLDTGEYSCEARNSVG.YRRCPGKRMQVDDLNISGIIAAVV

jam           245 VTLILLGLLIFGVWFAYSRGYFETTKKGTAPGKKVIYSQPSTRSEGEFKQ
35638         246 VVALVISVCGLGVCYAQRKGYF...SKETSFQKSNSSSKATTMSENVQWL

jam           295 TSSFLV
35638         293 TPVIPALWKAAAGGSRGQEF
```

FIG._17

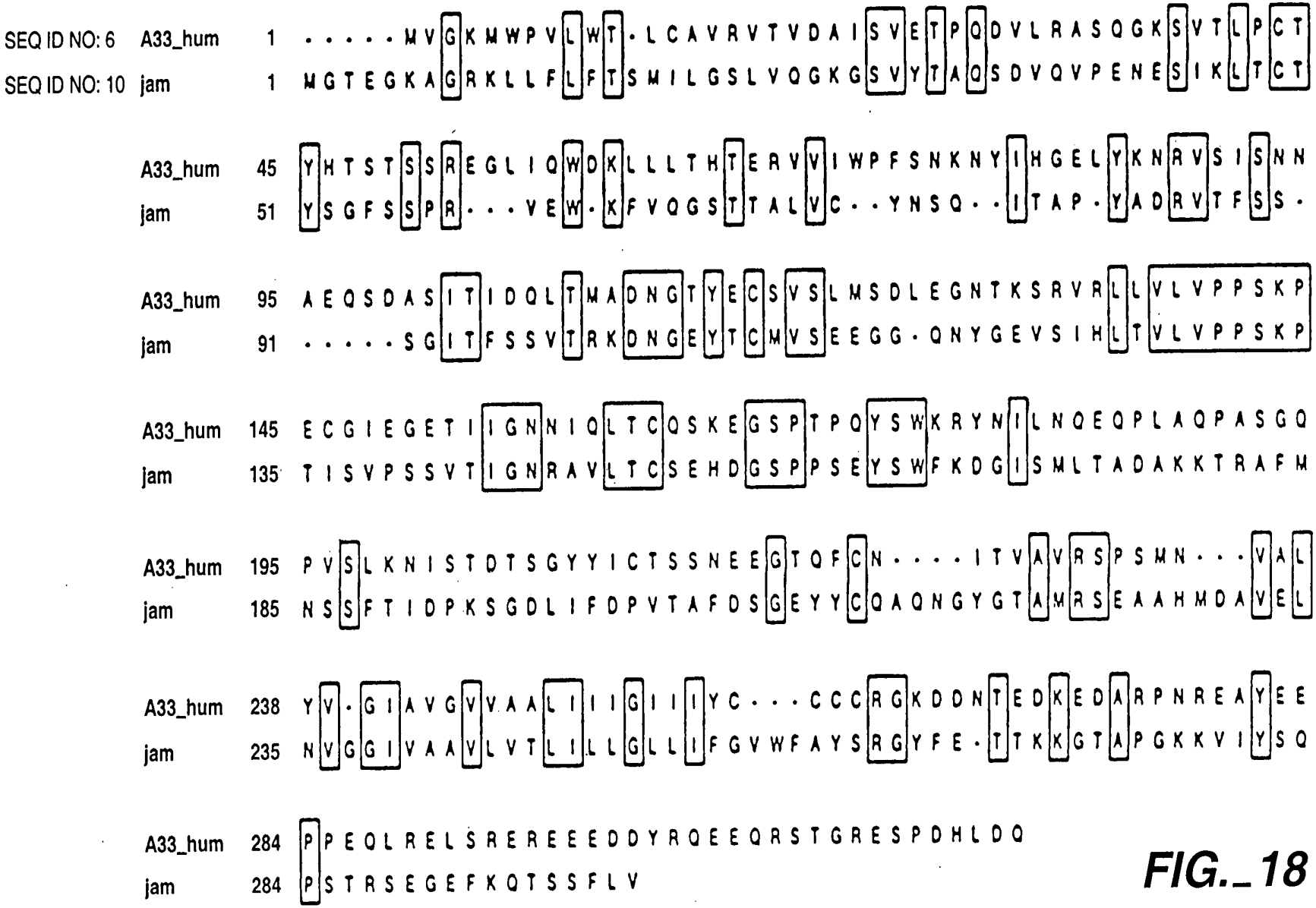
SEQ ID NO: 6 A33_hum 1 .....MVGKMWPVLWT·LCAVRVTVDAISVETPQDVLRASQGKSVTLPCT
SEQ ID NO: 10 jam 1 MGTEGKAGRKLLFLFTSMILGSLVQGKGSVYTAQSDVQVPENESIKLTCT
A33_hum 45 YHTSTSSREGLIQWDKLLLTHTERVVIWPFSNKNYIHGELYKNRVSISNN
jam 51 YSGFSSPR···VEW·KFVQGSTTALVC··YNSQ··ITAP·YADRVTFSS·
A33_hum 95 AEQSDASITIDQLTMADNGTYECSVSLMSDLEGNTKSRVRLLVLVPPSKP
jam 91 .....SGITFSSVTRKDNGEYTCMVSEEGG·QNYGEVSIHLTVLVPPSKP
A33_hum 145 ECGIEGETIIGNNIQLTCQSKEGSPTPQYSWKRYNILNQEQPLAQPASGQ
jam 135 TISVPSSVTIGNRAVLTCSEHDGSPPSEYSWFKDGISMLTADAKKTRAFM
A33_hum 195 PVSLKNISTDTSGYYICTSSNEEGTQFCN····ITVAVRSPSMN···VAL
jam 185 NSSFTIDPKSGDLIFDPVTAFDSGEYYCQAQNGYGTAMRSEAAHMDAVEL
A33_hum 238 YV·GIAVGVVAALIIIGIIIYC···CCCRGKDDNTEDKEDARPNREAYEE
jam 235 NVGGIVAAVLVTLILLGLLIFGVWFAYSRGYFE·TTKKGTAPGKKVIYSQ
A33_hum 284 PPEQLRELSRERFEEEDDYRQEEQRSTGRESPDHLDQ
jam 284 PSTRSEGEFKQTSSFLV

FIG._18

TISSUE	EXPRESSION
WHOLE BRAIN	+
AMYGDALA	+
CAUDATE NUCLEUS	+
CEREBELLUM	–
CEREBRAL CORTEX	+
FRONTAL LOBE	+
HIPPOCAMPUS	+
MEDULLA OBLONGATA	+
OCCIPITAL LOBE	+
PUTAMEN	+
SUSTANTIA NIGRA	+
TEMPORAL LOBE	+
THALAMUS	+
NUCLEUS ACCUMBEUS	+
SPINAL CORD	–

TISSUE	EXPRESSION
HEART	++
AORTA	+
SKELETAL MUSCLE	+
COLON	+++
BLADDER	++
UTERUS	+
PROSTATE	+++
STOMACH	+++
TESTIS	++
OVARY	+++
PANCREAS	++
PITUITARY GLAND	++
ADRENAL GLAND	++
THYROID GLAND	++
SALIVARY GLAND	+++
MAMMARY GLAND	++

TISSUE	EXPRESSION
KIDNEY	+++
LIVER	++
SMALL INTESTINE	++
SPLEEN	++
THYMUS	++
PERIPHERAL LEUKOCYTE	+
LYMPH NODE	+
BONE MARROW	+
APPENDIX	+
LUNG	++++
TRACHEA	++++
PLACENTA	++++
FETAL BRAIN	+
FETAL HEART	+
FETAL KIDNEY	++
FETAL LIVER	+++
FETAL SPLEEN	+
FETAL LUNG	++++

FIG._19

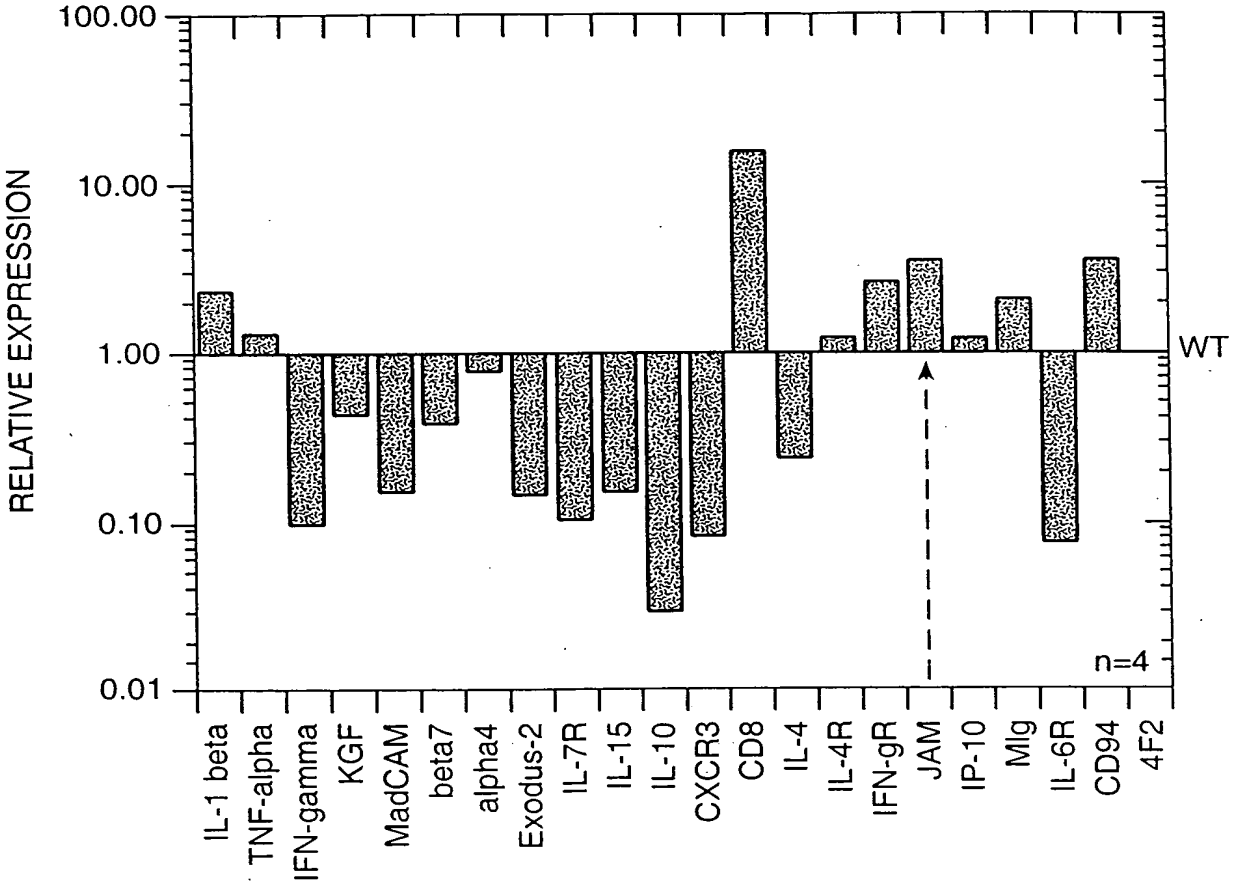
100.00
10.00
1.00
0.10
0.01
RELATIVE EXPRESSION
WT
n=4
IL-1 beta
TNF-alpha
IFN-gamma
KGF
MadCAM
beta7
alpha4
Exodus-2
IL-7R
IL-15
IL-10
CXCR3
CD8
IL-4
IL-4R
IFN-gR
JAM
IP-10
Mlg
IL-6R
CD94
4F2

FIG._20

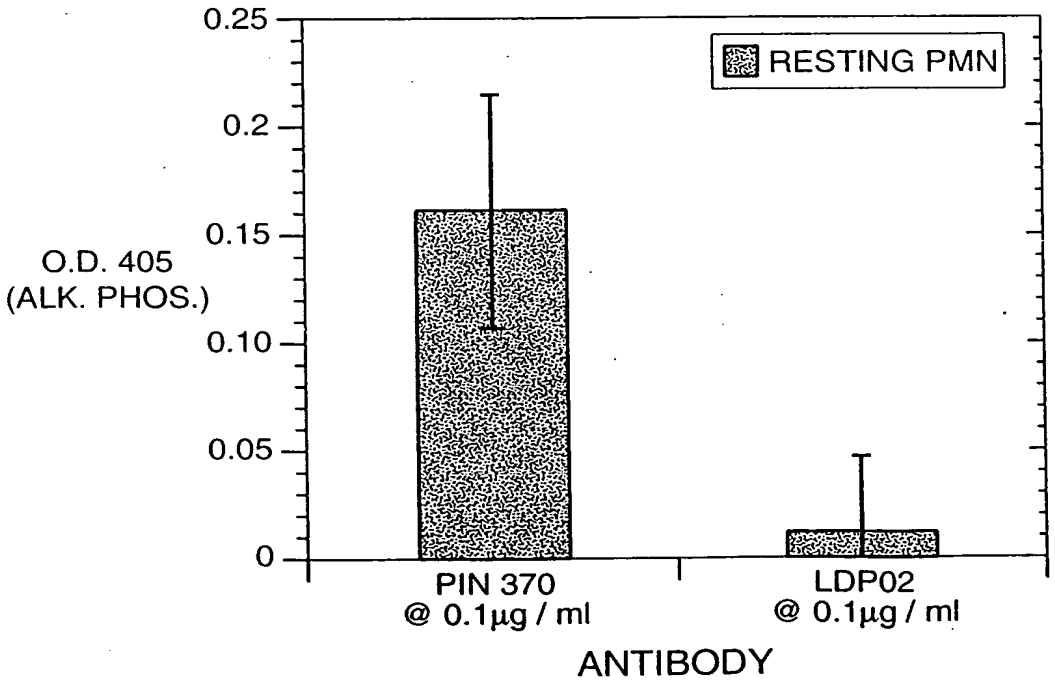
0.25
0.2
0.15
0.10
0.05
0
O.D. 405
(ALK. PHOS.)
RESTING PMN
PIN 370
@ 0.1µg / ml
LDP02
@ 0.1µg / ml
ANTIBODY

FIG._21